

#### **Blast 2 Sequences results**

Entrez

BLAST

OMIM

Taxonomy

Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 

gap open: 11 gap extension: 1

x\_dropoff: 50 expect: 10.00 wordsize: 3 Filter Align

Sequence 1 gi 3702836 hASIC3 [Homo sapiens] Length 531 Sequence 2 gi 13592019 P2X3 [Rattus norvegicus] Length 397 No significant similarity was found

# Align two sequences

# Tue Apr 15 17:04:02 BST 2003

/usr/tmp/seq1.214485.sca : 397 aa >gi 13592019 ref NP_112337.1  P2X3						
		10	2	0	30	40
/usr/t MNC	IS :	DFFTYETTK	SVVVK	SWTIG	GIINRAVQLL	IISYFVGW
	TSGPEEARRQPS	DIRVFASNO	:. :SMHGLGHVFG	 PGSLSLRRG	: : : : : : : : : : : : : : : : : : :	 Uatri Vou
				40	50	60
•		50	60		70	
/usr/t V	FLHEKA	YQVRDT	AIESSVVTKV	KGFGR	YANR	VMDVS
•	: :. :		· · · · · · · · · · · · · · · · · · ·	:		
g1 3/0 AER	VRYYREFHHQTA 70					ALLGLDPA
	70	80	90	100	110	120
80		90	100	110	120	130
/usr/t DYV	TPPQC	STSVFVIITE	IIVTENOMOG	FCPENEEKY	RCVSDSO-C	GPERFPGG
• • •	. ::	. :.				
g1   3 / U EHA	AFLRALGRPPAE 130	PPG-FMPSP1 140	'FDMAQLYARA	GHSLDDMLI		GPENFTTI
	130	140	150	160	170	
	140			150		
/usr/t GIL	TGRCVNYSS	VLRTC-		-EIQG	MC	PTEVD
ail270 pmp	······································	.: :		:	:	: ::
180	MGKCYTFNSGAL	GAELLTTTF	GGMGNGLDIM	LDVQQEEYI	LPVWRDNEET	PFEVGIRV
100	130	200	210	220	230	
	60	170	180		190	200
/usr/t	TVEMPIMME	AENFTI	FIKNSIR	FPLFNI	FEKGNLLPNL	TDKDIKRC
ai 1370 oth	· : :	· · ·	:	<u>: : .</u>	: ::	
240	SQEEPPIIDQLO 250	260	FVSCQQQQLS 270	FLPPPWGDO 280	CSSASLNPNY 290	-EPEPSDP
					290	
	210 2	220	230	240	250	260
/usr/t RFH	PEKAPFCPILR	GDVVKFAGO	DFAKLARTGG	VLGIKIGW-	VCDLDKA	WDQCIPKY
gi 370 LGS 300	: .: : . PSPSPSPPYTLM 310	.:: . MGCRLACE 320	T-RYVARKCG	CRMVYMPGI	::. DVPVCS-PQQ 340	: YKNC 350
	270	280	2	90		200
/usr/t SFT	RLDGVSEKSSVS	SPGYNFF	RFAKYYKM	ENGSEYRT	LLK	300
gi 370 AHPAIDAILRKDSCACPNPCASTRYAKELSMVRIPSRAAARFLARKLNRSEAYIAENVLA						
STISTO ARP	360	ACPNPCASTE 370	YAKELSMVRI 380	PSRAAARF1 390	LARKLNRSEA 400	YIAENVLA 410

Sequence Alignment Output

4/15/03 12:05 PM

310 .320 330 340 /usr/t FGIRFDVLVYGNAGK-----FNIIPTIISSVAAFTSVGVGTVL-----CDII---LLN gil370 LDIFFEALNYETVEQKKAYEMSELLGDIGGQMGLFIGASLLTILEILDYLCEVFRDKVLG 420 430 440 450 470 350 360 370 380 390 /usr/t FLKGADHYKARKFEEVTETTLKGTASTN-----PVFASDQATVEKQSTDSG--AYSIG gil370 YFWNRQHSQRHSSTNLLQEGL-GSHRTQVPHLSLGPRPPTPPCAVTKTLSASHRTCYLVT 480 490 500 510

/usr/t H-

gi|370 QL 530

Elapsed time: 0:00:00

Blast Result

4/15/03 11:45 AM



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Matrix BLOSUM62 ♦ gap open: 11 gap extension: 1

x\_dropoff: 50 expect: 10.00 wordsize: 3 Filter Align

Sequence 1 gi 3702836 proton-gated cation channel subunit [Homo sapiens] Length 531

Sequence 2 gi 12643353 P2X purinoceptor 2 (ATP receptor) (P2X2) (Purinergic receptor) Length 471

N significant similarity was found

### Align two sequences

### Tue Apr 15 18:49:23 BST 2003

/usr/tmp/seq1.215975.sca : 472 aa >gi 1352688 sp P49653 P2X2_RAT_P2X_purinoceptor 2						
/usr/t M-		10 VRRLARGC-W	2	0	30	40
:		.: .: .:	:			
g1 3/0 MK	PTSGPEEARRQP: 10	SDIRVFASNCSM 20	HGLGHVFGF 30	GSLSLR-F 40	RGMWAAAVY 50	
4 4	50	60		70	80	
/usr/t V-	WYVFIVQ	KSYQDSETG	-PESSII	TKVKGIT	ISEDKV-WI	OVEEYVKP
gi 370 VA	ERVRYYREFHHQ:	raldereshrlv	FPAVTLCNI	 NPLRRSRI	LTPNDLHW	. : AGSALLGLDP
60	70	80	90	100	110	)
90	100				140	)
/usr/t PE	GGSVVSIITRIE	VTPSQTLGTCPE	SMRVHSSTC	CHSDDDCIA	AGQLDMQG1	NGIRTGHCVP
gil370 AE	HAAFLRALGRPP	APPGFMPSPTFD	MAQLYARAG	HSLDDML	:: . LDCR	.: : : FRGQPCGP
120	130	140		160		170
150 /usr/t YY	160 HGDSKTCEVSAW	170 CPVEDGTSDNHF	LGKN	APNFTIL-	IKNSIH	200 YPKFKFSKGN
	Fttiftrmgk	::.	: ::			· ·
92,370 214	180	190	200	210	220	LPVWRDN
/usr/t IA	210 SQKSDYLKHCTF	220 2 DQDSDPYCPIFR	30 LGFIVEKAG	240 SENFTELAI	250 HKGGVIGV	260 IINWNCDLDI.
		.:. : : .	::. : .	:.		· · ·
230	TPFEVGIRVQIH 240	SQEEPPIIDQ 250	LGLGVSPG) 260			PPPWGDC 280
/usr/t SE	270 SECNPKYSFRRL	DPKYDPASSGYN	90 IFRFAKYYKI	300 [NGTT	31( TTRTLIKA	YGIRIDVIVH
:	. :::: .	:: .:. :	. : .		::	
911370 55	ASLNPNYEPEPS 290	300	SPPYTI 310	LMGCRLACI 320		CGCRM-VYMP 330
	330			360	3'	70
/usr/t GQ	AGKFSLIPTIIN	LATALTSI-GVG	SFLCDWILI	LTFMNKNK		
	•	· • • •	: :	•	:. :	:: :
3	VPVCSPQQYKNC 40 350	AHPAIDAILRKE 360	SCACPNPCA 370	ASTR	-YA-KELS 380	MVRIPSRAAA 390

Sequence Alignment Output

4/15/03 1:50 PM

. 3	380	390	400	410		420
/usr/t	RWPVTLA	ALVLGQI	PPPSHYSQDQ	PPSPPSGE-	GPTLGI	EGAEL
•	: :		:			:: :
gi 370	RFLARKLNRSEAYIA			KKAYEMSEL	LGDIGGQMG:	LFIGASL
	400	410	420	430	440	450
	430			440		450
/usr/t	PLAVQS-PRPCSI		SALTE	QVVDTLGQH	M	GQRPPVP
	•• • • •			::::		: :::::
gi 370	LTILEILDYLCEVF	RDKVLGYFWN	RQHSQRHSSTN	ILLQEGLGSH	RTQVPHLSL	GPRPPTP
	460	470	480	490	500	510
	460	470				
/usr/t	EPSQQDSTSTDPKG-	LAQL				
	:	::				
gi 370	PCAVTKTLSASHRT	CYLVTQL				
	520	530				
Elansed	time: 0.00.00	`				